

Application No. 09/857,315
Amdt. dated September 8, 2006
Reply to Office Action of June 8, 2006

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Having regard thereto, it is submitted that claims 19, 22 and 24 to 28 are no longer open to provisional rejection under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 19, 20, 22 and 24 to 28 of co-pending Application no. 10/699,683 and hence the rejection should be withdrawn.

The Examiner rejected claims 19, 22, 24, 25, 27 and 28 under 35 U.S.C. 102(e) as being anticipated by Murdin et al U.S. Patent nos. 6,693,087 or 6,686,339. Reconsideration is requested.

The Examiner states that:

"Murdin et al., for example 6,696,087 (the Examiner means 6,693,087) discloses a nucleic acid molecule encoding an outer membrane protein (MOMP) of a strain of *Chlamydia* (abstract)."

The abstract of Murdin et al 6,693,087 states:

"An isolated and purified nucleic acid molecule encoding a POMP91A protein of a strain of *Chlamydia*..." (emphasis added)

The abstract does not mention MOMP but rather a quite different protein of *Chlamydia*. Similarly, the "Abstract" of Murdin et al 6,686,339 states:

"....method of nucleic acid,.... immunization of a host,....employing a vector, containing a nucleotide sequence encoding an inclusion membrane protein C of a strain of *Chlamydia*...." (emphasis added)

This inclusion membrane protein C to which Murdin et al 6,686,339 relates is a further, different protein from MOMP.

Enclosed for the Examiner's consideration is a sequence comparison for the amino acid sequences from the MOMP, POMP91A and InC proteins of *Chlamydia pneumoniae*. The sequence comparison was prepared using the CLUSTAL W (1.83) multiple sequence alignment at the default settings. For the

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convenience of the Examiner, enclosed are the annotated sequences used to prepare the alignments. It can be seen that there is no similarity among the three sequences.

The Examiner does not indicate in the Office Action wherein is the Murdin et al reference there is disclosed a vector comprising a nucleic acid molecule encoding MOMP. It is submitted that the only vectors disclosed are molecules containing the nucleic acid molecule encoding POMP91 (US 6,693,087) or encoding inclusion membrane protein C (US 6,686,339).

Accordingly, it is submitted that applicant's pending claims are not anticipated by either Murdin et al reference and hence the rejection of claims 19, 22, 24, 25, 27 and 28 under 35 U.S.C.102(e) as being anticipated by Murdin et al (6,693,087 or 6,686,339), should be withdrawn.

The Examiner rejected claim 26 under 35 U.S.C. 103(a) over Murdin et al. (6,693,087 or 6,686,339) as applied to claims 19, 22, 24, 25, 27 and 28 and further in view of Brunham (WO 98/02546). Claim 26 is dependent, indirectly, on claim 19 and recites that the plasmid vector is pcDNA3/MOMP.

The Murdin et al references have been discussed above. As set forth in that discussion, the Murdin et al reference does not disclose a vector comprising a nucleic acid molecule encoding MOMP.

Brunham describes the vector pcDNA3/MOMP, there is no motivation provided by Brunham or Murdin et al to substitute this vector for the vectors described in Murdin in an attenuated bacterium environment.

Accordingly, it is submitted that claim 26 is patentable over the applied art and hence the rejection thereof under 35 U.S.C. 103(a) as being unpatentable over either Murdin et al reference in view of Brunham, should be withdrawn.

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It is believed that this application is now in condition for allowance and early and favourable consideration and allowance are respectfully solicited.

Respectfully submitted,



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! Sequence: momp
! Sequence: incC
! Sequence: pomp91a
CLUSTAL W (1.83) multiple sequence alignment

```

momp      -----
incC      -----
pomp91a   MIQMRLWGFILSSFCQVSYLRANDVLLPLSGIHSGEDLELFTLRSSSPTKTTYSLRKDF

                                     MKKLLKSVLVFAALSSASSLQALFVG--
momp      -----
incC      -----
pomp91a   IVCDFAGNSIHKPGAFLNLKGDLEFFINSTFLAALTFKNIHLGARGAGLFESNVTFKGL
                                     : : :

                                     NPAEPSLMIDGILWEGFGGDPDCPCATWCDASIMRVGYGDFVF
momp      -----
incC      -----
pomp91a   HSLVLENNE SWGGVLTTS GDLSFINNTSVLCQNNISYGPGGALLQGRKSKALFFRDNRG
                                     : : :

DQVLKTDVNKEFQMGAKPTTDTGNSAAPS-----
incC      -----
pomp91a   QADRLEPTASIILOVGGAPTGGGACAPFQPG-----
                                     TILFLKNKAVNQDESHPGYGGAVSSISPGSPITFADNQEILFOENEGELGGAIYNDQGA
                                     : : :

                                     TLTARENPAYGRHMQDAEMFTNAACMALNIWDR--
momp      -----
incC      -----
pomp91a   TFBNNFQTTSFSSNKASFEELSIAATAISIHSGAIPYSLKTLLOKLGGATHADYVHIRDC
                                     : : :

FDFVCTLGATSGYLKGNASAFNLVGLFGDNENQKTVKAESVPMMSFDQSVVELYTDTT
incC      -----
pomp91a   STLQQSTKGARTGVLVVTAILMTISLLAIIIIILAVLGFTG---VLPOVALLMQGETN
                                     HGSIVFEENSATAGGATAVNAVCDINAQGFVRFINNSALGLNGGAIYMQATGSILALHAN
                                     : : :

                                     FAWSVGARAALWECGCATLG---
momp      -----
incC      -----
pomp91a   QGDIEFCGNKVRSQFHSHINSTSNFTNNAITIQAPREFSLSANEGHRICFYDPIISATE
                                     : : :

momp      -----
incC      -----
pomp91a   GYNLYINHQRLLLEAGGAVIFSGARLSPEHKKENKNKTSIINQPVRLCSGVLSIEGGAIL

                                     ASFOYAQSKPKVEELNVLNAAEF
momp      -----
incC      -----
pomp91a   AVRSFYQEGGLLALGPGSKLTQGNSEKDKIVITNLGFNLNLDSSDPAEIRATEKASI
                                     : : :

PINKPKGYVGKEFPLOLTAGTDAATG-----
incC      -----
pomp91a   EISGVPRVYGHTESFYENHEYASKFYTTSIILSAKKLVTA PSRPEKDIQNLIIAESEYMG

                                     TKDASIDYHEWQASLALSYRLNMFTPYIGVKWSRASFDADTIRIA
momp      -----
incC      -----
pomp91a   YGYQGSWEFSWSFNDTKEKKTIIASWTPTGFEFLDPKRRGSFPTTLWSTFSGLNIAJNI

QPKSATAIFDTTTLNPTIAGAGDVKTGAEGQLGDTMQIVSLQLNKMKSRSKSGIAVGTTI
incC      -----

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pomp91a	VNNNYLNNSEVIPLQHL CVFGGFVYQIMEQNPKQSSNNLLVQHAGHNVGARIPFSFNTIL
momp	VCADKYAVTVETRLIDERA AHVNAQFRF-----
incC	-----
pomp91a	SPALTQLFSSSSQONVADKSHAQILIGTVSLNKSQALSLRSSFSYTEDSQVMKHVFPYK
momp	-----
incC	-----
pomp91a	G)SRGSWRNYGWSGSVGM SYAYPKGIRYLKMTPFVDLQYTKLVQNPFVETGYDPRYFSSS
momp	-----
incC	-----
pomp91a	EMTNLSLPIGIALEMRFIGSRSSSLFLQVSTSYIKOLRRVNPQSSASLVLNHYTWDIQGVF
momp	-----
incC	-----
pomp91a	LGKEALNITLNSTIKYKIVTAYMGISSTQREGSNLSANAHAGLSLSF

"*" means that the residues or nucleotides in that column are identical in all sequences in the alignment
 "." means that conserved substitutions have been observed
 "-" means that semi-conserved substitutions are observed

6693087pomp91a seq
947 aa linear PAT 20-FEB-2004

LOCUS AAS37561
DEFINITION Sequence from patent US 6693087.
ACCESSION AAS37561
VERSION AAS37561.1 GI:42715796
DBSOURCE accession AAS37561.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (residues 1 to 947)
AUTHORS Murdin,A.D., Dunn,P.L. and Oomen,R.P.
TITLE Nucleic acid molecules encoding POMP91A protein of Chlamydia
JOURNAL Patent: US 6693087-A 3 17-FEB-2004;
Aventis Pasteur Limited; Toronto;
CAX;
REMARK CAMBIA Patent Lens: US 6693087
FEATURES Location/Qualifiers
source ..947
/organism="unknown"

ORIGIN

1	mkqmrllwgfl	flssfcqvsv	lrandvllpl	sgihsgedle	lftlrssst	kttylrlkdf
61	ivcdfagnsi	hkpgaafnl	kgdlffinst	plaaalfkni	hlqargaglf	sesnvtfkgf
121	hslvlennes	wggvlttsd	lsfinntsvl	cnnnisypg	galllqgrks	kalffrdnrg
181	tilflknkav	ngdeshpgyg	gavssispgs	pitfadnqei	lfgenegeig	gaiyndggai
241	tfennfqttt	ffsnkastee	lsiaataisi	hsgaipyslk	tlqlklggai	hadyvhirdc
301	kgsivfeens	ataggaiavn	avcdinaqgp	vrfinnsalg	lmggaiymqa	tgsilrlhan
361	qgdiefcgnk	vrsqfhshin	stsnftnnai	tiqgaprefs	lsaneghric	fydpiisate
421	nynslyinhq	rlleaggavi	fsgarlspch	kkenknktsi	inqpvrllcs	visieggail
481	ayrsfyqegg	llaalpggskl	ttqgknsekd	kivitnlqfn	lenldssdpa	eiratekasi
541	eisgvprvyg	htesfyenhe	yaskpyttsi	ilsakkllvta	psrpekdiqn	liiaeseymg
601	ygyqgsweff	wspndtkekk	tiiaswtptg	efslpkrrg	sfipptllwt	fsglniasni
661	vnnnylnnse	viplqlcvf	ggpvvgimeq	npkqssnnll	vqhaghnvga	ripfsfntil
721	saaltqlfss	ssqnvadks	haqiligtvs	lnkswgalsl	rssfsyteds	qvmkhvfpyk
781	gtsrgswrny	gwsqsvqmsy	aypkgyrylk	mtpfvdlqyt	klvqnpfvct	gydpryfsst
841	emtnlslpig	ialemrfigs	rsslflqvst	syikdlrrvn	pqssaslvl	hytwdiqgvp
901	lgkealniti	nstikyki	aymgisstqr	egsnlsanah	aglsisf	

66863391ncc seq 203 aa linear PAT 20-FEB-2004

LOCUS AAS33023
 DEFINITION Sequence from patent US 6686339.
 ACCESSION AAS33023
 VERSION AAS33023.1 GI:42707452
 DBSOURCE accession AAS33023.1
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (residues 1 to 203)
 AUTHORS Murdin,A.D., Dunn,P.L. and Oomen,R.P.
 TITLE Nucleic acid molecules encoding inclusion membrane protein C of
 Chlamydia
 JOURNAL Patent: US 6686339-A 3 03-FEB-2004;
 Aventis Pasteur Limited; Toronto;
 CAX;
 REMARK CAMBIA Patent Lens: US 6686339
 FEATURES Location/Qualifiers
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ORIGIN
 1 mtspipfqs gdsflaeqp qqlpstsesq lvtqlltmmk htgalsetvl qqqrdr1pta
 61 siilqvvgap eggagapfqp gpaddhhhpi pppvvpqie teittirsel qlmrstlqqs
 121 tkgartgvlv vtailmtisl laiiiiiilav lgftgvlpqv allmqgetnl iwamvsgsli
 181 cfialigtlg liltknkntpl pas

stephens momp
393 aa linear BCT 02-MAY-2006

LOCUS Q46409
DEFINITION Major outer membrane protein, serovar D precursor (MOMP).
ACCESSION Q46409
VERSION Q46409 GI:6707730
DBSOURCE swissprot: locus OM1D_CHLTR, accession Q46409;
class: standard.
created: May 30, 2000.
sequence updated: Nov 1, 1996.
annotation updated: May 2, 2006.
xrefs: X62918.1, CAA44701.1, AF063195.2, AAC31436.2, AE001273.1,
AAC68276.1, H71484
xrefs (non-sequence databases): PHCI-2DPAGE:Q46409,
GenomeReviews:AE001273_GR, InterPro:IPR000604, Pfam:PF01308,
PRINTS:PR01334

KEYWORDS Complete proteome; Ion transport; Membrane; Outer membrane; Porin;
Signal; Transmembrane; Transport.

SOURCE Chlamydia trachomatis
ORGANISM Chlamydia trachomatis
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

REFERENCE 1 (residues 1 to 393)
AUTHORS Sayada, C., Denamur, E. and Elion, J.
TITLE Complete sequence of the major outer membrane protein-encoding gene
of Chlamydia trachomatis serovar Da
JOURNAL Gene 120 (1), 129-130 (1992)
PUBMED 1398119
REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=D/B-120

REFERENCE 2 (residues 1 to 393)
AUTHORS Stothard, P.R., Boguslawski, G. and Jones, R.B.
TITLE Phylogenetic analysis of the Chlamydia trachomatis major outer
membrane protein and examination of potential pathogenic
determinants
JOURNAL Infect. Immun. 66 (8), 3618-3625 (1998)
PUBMED 9673241
REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=D/IU-71960

REFERENCE 3 (residues 1 to 393)
AUTHORS Stephens, R.S., Kalman, S., Lammel, C., Fan, J., Marathe, R.,
Aravind, L., Mitchell, W., Olinger, L., Tatusov, R.L., Zhao, Q.,
Koonin, E.V. and Davis, R.W.
TITLE Genome sequence of an obligate intracellular pathogen of humans:
Chlamydia trachomatis
JOURNAL Science 282 (5389), 754-759 (1998)
PUBMED 9784136
REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=D/UW-3/Cx

COMMENT On Sep 27, 2005 this sequence version replaced gi:7442973.
[FUNCTION] Structural rigidity of the outer membrane of elementary
bodies and porin forming, permitting diffusion of solutes through
the intracellular reticulate body membrane.
[SUBUNIT] Disulfide bond interactions within and between MOMP
molecules and other components form high molecular-weight
oligomers.
[SUBCELLULAR LOCATION] Bacterial cell outer membrane; multi-pass
membrane protein.
[SIMILARITY] Belongs to the chlamydial OMP family.

FEATURES
source Location/Qualifiers
1..393
/organism="Chlamydia trachomatis"
/db_xref="taxon:813"
gene 1..393
/gene="ompA"
/locus_tag="CT_681"

stephens momp
Protein /note="synonym: omp1"
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/gene="ompA"
/locus_tag="CT_681"
/product="Major outer membrane protein, serovar D
precursor"
Region 1..22
/gene="ompA"
/locus_tag="CT_681"
/region_name="Signal"
/inference="non-experimental evidence, no additional
details recorded"
Region 23..393
/gene="ompA"
/locus_tag="CT_681"
/region_name="Mature chain"
/experiment="experimental evidence, no additional details
recorded"
/note="Major outer membrane protein, serovar D.
/FTId=PRO_0000020147."

ORIGIN
1 mkkllksvly faalssassl qalpvgnpae pslmidgilw egfggdpcdp catwcdaism
61 rvgyygdvfv drvlktdvnk efqmgakptt dtgnsaapst ltarenpayg rhmqdaemft
121 naacmalniw drfdvfcrlg atsgylkgnv asfnlvglfg dnengktvka esvpmnsfdq
181 svveltydtl fawsvgaraa lwecgcrlg asfqyagskp kveelnlcn aaftinkpk
241 gyvgkefpld ltagtdaatg tkdasidyhe wqasialsy lnmftpyigv kwsrasfdad
301 tiriaqpkas taifdtttln ptiagagdvk tgaegqlgdt mqivslqlnk mksrkscgia
361 vgttividak yavtvetrli deraahvnaq frf

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